PCT10

RAW SEQUENCE LISTING DATE: 06/21/2002
PATENT APPLICATION: US/10/019,633 TIME: 11:46:04

Input Set : A:\BB1386 US PCT substitute sequence listing.txt
Output Set: N:\CRF3\06212002\J019633.raw

<110> APPLICANT: Caspar, Timothy
Falco, Saverio Carl
Sakai, Hajime
Weng, Zude
Hu, Xu

<120> TITLE OF INVENTION: PURINE METABOLISM GENES IN PLANTS

<130> FILE REFERENCE: BB-1386

<140> CURRENT APPLICATION NUMBER: 10/019,633

C--> <141> CURRENT FILING DATE: 2002-05-28

<150> PRIOR APPLICATION NUMBER: 60/146,473

<151> PRIOR FILING DATE: 1999-07-30

<160> NUMBER OF SEQ ID NOS: 24

<170> SOFTWARE: Microsoft Office 97

<210> SEQ ID NO: 1

<211> LENGTH: 1910

<212> TYPE: DNA

<213> ORGANISM: Zea mays

<400> SEQUENCE: 1

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gttgatggcg ttatccatgt ttatgcggat aaagattgta cggagagcat ttatcctgtg 180
gctgatgcta caaccttctt cactgacttg cattatattc tccgagtaac ggctgcaggg 240
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ctgatgttaa atgcggatag ggaatttctt gcccagaaga ctgccccaca tcgtgatttt 360
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ttccaaaatc ttcttgacaa cattttcgtt cctcttttg aggttactat tgatccagct 960
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54 tcttgtgatt tatgcgaaat tgcgaggaac tctgtttacc aatctgggtt ttcacatgct 1560
55 ctcaaggcgc actggattgg taagaactac ttcaaaagag gacctgctgg aaatgatatt 1620
56 cacagaacca atgtaccgca catcagggtt caatttagag agatgatctg gagaaatgaa 1680
57 atgaaactag tgtactctga caatgagatc ttaataccag acgagctgga cctgtaagat 1740
58 gtccagcctc gtgtatacca gacgagttgc gttgtagctg ctatgggaat tatacttcat 1800
59 gttttggtat gctttcctta tctatggcaa attcaacttc gaacttcaaa aaaaaaaaaa 1860
60 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1910
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 578
64 <212> TYPE: PRT
65 <213> ORGANISM: Zea mays
67 <400> SEQUENCE: 2
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69 1 5 10 15
71 Cys Thr Pro Lys Pro Asn Pro Asn Pro Phe Thr Tyr Val Pro Glu Pro
72 20 25 30
74 Lys Ser Glu His Val Phe Gln Thr Val Asp Gly Val Ile His Val Tyr
75 35 40 45
77 Ala Asp Lys Asp Cys Thr Glu Ser Ile Tyr Pro Val Ala Asp Ala Thr
78 50 55 60
80 Thr Phe Phe Thr Asp Leu His Tyr Ile Leu Arg Val Thr Ala Ala Gly
81 65 70 75 80
83 Asn Thr Arg Thr Val Cys His Asn Arg Leu Asn Leu Leu Glu His Lys
84 85 90 95
86 Phe Lys Phe His Leu Met Leu Asn Ala Asp Arg Glu Phe Leu Ala Gln
87 100 105 110
89 Lys Thr Ala Pro His Arg Asp Phe Tyr Asn Val Arg Lys Val Asp Thr
90 115 120 125
92 His Val His His Ser Ala Cys Met Asn Gln Lys His Leu Leu Arg Phe
93 130 135 140
95 Ile Lys Ser Lys Leu Arg Lys Glu Pro Asp Glu Val Val Ile Phe Arg
96 145 150 155 160
98 Asp Gly Thr Tyr Met Thr Leu Lys Glu Val Phe Glu Ser Leu Asp Leu
99 165 170 175
101 Thr Gly Tyr Asp Leu Asn Val Asp Leu Leu Asp Val His Ala Asp Lys
102 180 185 190
104 Ser Thr Phe His Arg Phe Asp Lys Phe Asn Leu Lys Tyr Asn Pro Cys
105 195 200 205
107 Gly Gln Ser Arg Leu Arg Glu Ile Phe Leu Lys Gln Asp Asn Leu Ile
108 210 215 220
110 Gln Gly Arg Phe Leu Ala Glu Leu Thr Lys Gln Val Phe Ser Asp Leu
111 225 230 235 240
113 Ser Ala Ser Lys Tyr Gln Met Ala Glu Tyr Arg Ile Ser Ile Tyr Gly
114 245 250 255
116 Arg Lys Gln Ser Glu Trp Asp Gln Leu Ala Ser Trp Ile Val Asn Asn
117 260 265 270
119 Glu Leu His Ser Gly Asn Val Val Trp Leu Val Gln Ile Pro Arg Leu
120 275 280 285
122 Tyr Asn Val Tyr Lys Glu Met Gly Ile Val Thr Ser Phe Gln Asn Leu

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126 305                 310                 315                 320
128 Ser His Pro Gln Leu His Val Phe Leu Lys Gln Val Val Gly Leu Asp
129                 325                 330                 335
131 Leu Val Asp Asp Glu Ser Lys Pro Glu Arg Arg Pro Thr Lys His Met
132             340                 345                 350
134 Pro Thr Pro Glu Gln Trp Thr Asn Val Phe Asn Pro Ala Phe Ser Tyr
135         355                 360                 365
137 Tyr Ala Tyr Tyr Cys Tyr Ala Asn Leu Phe Thr Leu Asn Lys Leu Arg
138     370                 375                 380
140 Glu Ser Lys Gly Met Thr Thr Ile Lys Phe Arg Pro His Ala Gly Glu
141 385                 390                 395                 400
143 Ala Gly Asp Val Asp His Leu Ala Ala Thr Phe Leu Leu Cys His Asn
144                 405                 410                 415
146 Ile Ser His Gly Ile Asn Leu Arg Lys Ser Pro Val Leu Gln Tyr Leu
147             420                 425                 430
149 Tyr Tyr Leu Gly Gln Ile Gly Leu Ala Met Ser Pro Leu Ser Asn Asn
150         435                 440                 445
152 Ser Leu Phe Leu Asp Tyr His Arg Asn Pro Phe Pro Thr Phe Phe Gln
153     450                 455                 460
155 Arg Gly Leu Asn Val Ser Leu Ser Thr Asp Asp Pro Leu Gln Ile His
156 465                 470                 475                 480
158 Leu Thr Lys Glu Pro Leu Val Glu Glu Tyr Ser Ile Ala Ala Ser Leu
159                 485                 490                 495
161 Trp Lys Leu Ser Ser Cys Asp Leu Cys Glu Ile Ala Arg Asn Ser Val
162             500                 505                 510
164 Tyr Gln Ser Gly Phe Ser His Ala Leu Lys Ala His Trp Ile Gly Lys
165         515                 520                 525
167 Asn Tyr Phe Lys Arg Gly Pro Ala Gly Asn Asp Ile His Arg Thr Asn
168     530                 535                 540
170 Val Pro His Ile Arg Val Gln Phe Arg Glu Met Ile Trp Arg Asn Glu
171 545                 550                 555                 560
173 Met Lys Leu Val Tyr Ser Asp Asn Glu Ile Leu Ile Pro Asp Glu Leu
174                 565                 570                 575
176 Asp Leu
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180 <211> LENGTH: 1816
181 <212> TYPE: DNA
182 <213> ORGANISM: Oryza sativa
184 <400> SEQUENCE: 3
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186 ccgatagaga actacttgct cagaaagctg caccccatcg ggacttctac aatgtcagga  120
187 aggttgatac tcatgttcat cactctgcat gcatgaatca gaagcatctg ttgagattta  180
188 tcaagtccaa gttgaggaaa gaacctgacg aggttgtgat ttttagagat ggtacctatt  240
189 tgactcttaa ggaggttttt gagagtttgg acttgactgg ttatgacctc aatgttgatc  300
190 tcttagatgt gcatgccgat aaaagtacat tccatcgctt tgacaagttc aatttgaagt  360
191 ataatccttg tggccaatcc cggctgaggg agatctttct taaacaggac aaccttattc  420
192 aaggccgatt tcttgctgaa ttgacaaaag aagtattttc tgatcttgaa gcaagtaaat  480
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RAW SEQUENCE LISTING DATE: 06/21/2002
PATENT APPLICATION: US/10/019,633 TIME: 11:46:04

Input Set : A:\BB1386 US PCT substitute sequence listing.txt
Output Set: N:\CRF3\06212002\J019633.raw

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193 atcagatggc tgagtataga atatctatct atgggagaaa gaaaagtgag tgggatcaga  540
194 tggcaagctg gatagtgaat aatgaattgt acagcgagaa tgttgtttgg ttaattcaga  600
195 ttcctcggat atacaatgta tacagggaga tgggaacaat caattctttc cagaacctcc  660
196 ttgacaatat ttttctgcct ctttttgaag taactgttga tcctgcttca catcctcagc  720
197 tccatgtttt cttgcaacag gtcgttgggc tggatttagt ggatgatgaa agcaaaccag  780
198 agagacgccc aacaaaacac atgcctacac ctgagcaatg gactaatgtt ttcaatccag  840
199 catatgcata ttatgtgtac tattgttatg ctaacttgta cacgctgaac aagcttcgtg  900
200 agtccaaggg tatgacaaca atcaaacttc gtccacactg tggggaggct ggagatattg  960
201 atcatcttgc tgcagcattt cttacttctc ataatattgc tcacggggtt aatttaaaga 1020
202 agtcccctgt cctccagtat ctgtattacc tagctcagat tggtcttgcc atgtctcctt 1080
203 tgagcaacaa ctcaatgttt attgattatc accgaaaccc tttcccaaca tttttcctaa 1140
204 gaggccttaa cgtttctcta tcaaccgatg acccttttgca aattcacctg acaaaagaac 1200
205 ctttggttga agaatatagc atcgctgctt cgctgtggaa gctaagttca tgcgacctat 1260
206 gtgaaattgc taggaattct gtgtaccagt ctggtttctc tcataggctc aagtcacact 1320
207 ggattgggag aaactactac aaaagaggtc atgatggcaa tgacattcac cagacaaatg 1380
208 ttcctcacat caggattgaa ttccgacaca ctatttggaa agaagaaatg gagctaatac 1440
209 atctgaggaa tgttgatata ccggaagaaa ttgataggtg aagacctggc aagaattttg 1500
210 caaaccctga agttacttgg ttgttgatga tggtcctgga aggcacccca tcttcctacc 1560
211 ataaactttc caggtacaac caagaccgtg cggtttctac ttgcttgcgg aagggaggag 1620
212 aaagggatct aggatgattc tacttttcga tgaatctccg tagcgtgttg cgttccctag 1680
213 tagtaggatt ttgataaaag aaattatgtt aggactgagg ccgtaccata aaataagaaa 1740
214 gatttgagtc atggaatact ggaagtttaa acataaaaaa aaaaaaaaaa aaaaaaaaaa 1800
215 aaaaaaaaaa aaaaaa                                                1816
217 <210> SEQ ID NO: 4
218 <211> LENGTH: 492
219 <212> TYPE: PRT
220 <213> ORGANISM: Oryza sativa
222 <400> SEQUENCE: 4
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226 Met Val Asn Ala Asp Arg Glu Leu Leu Ala Gln Lys Ala Ala Pro His
227              20                  25                  30
229 Arg Asp Phe Tyr Asn Val Arg Lys Val Asp Thr His Val His His Ser
230          35                  40                  45
232 Ala Cys Met Asn Gln Lys His Leu Leu Arg Phe Ile Lys Ser Lys Leu
233      50                  55                  60
235 Arg Lys Glu Pro Asp Glu Val Val Ile Phe Arg Asp Gly Thr Tyr Leu
236 65                  70                  75                  80
238 Thr Leu Lys Glu Val Phe Glu Ser Leu Asp Leu Thr Gly Tyr Asp Leu
239                 85                  90                  95
241 Asn Val Asp Leu Leu Asp Val His Ala Asp Lys Ser Thr Phe His Arg
242             100                 105                 110
244 Phe Asp Lys Phe Asn Leu Lys Tyr Asn Pro Cys Gly Gln Ser Arg Leu
245         115                 120                 125
247 Arg Glu Ile Phe Leu Lys Gln Asp Asn Leu Ile Gln Gly Arg Phe Leu
248     130                 135                 140
250 Ala Glu Leu Thr Lys Glu Val Phe Ser Asp Leu Glu Ala Ser Lys Tyr
251 145                 150                 155                 160
253 Gln Met Ala Glu Tyr Arg Ile Ser Ile Tyr Gly Arg Lys Lys Ser Glu
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PATENT APPLICATION: US/10/019,633 TIME: 11:46:04

Input Set : A:\BB1386 US PCT substitute sequence listing.txt
Output Set: N:\CRF3\06212002\J019633.raw

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257             180                 185                 190
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260         195                 200                 205
262 Glu Met Gly Thr Ile Asn Ser Phe Gln Asn Leu Leu Asp Asn Ile Phe
263     210                 215                 220
265 Leu Pro Leu Phe Glu Val Thr Val Asp Pro Ala Ser His Pro Gln Leu
266 225                 230                 235                 240
268 His Val Phe Leu Gln Gln Val Val Gly Leu Asp Leu Val Asp Asp Glu
269                 245                 250                 255
271 Ser Lys Pro Glu Arg Arg Pro Thr Lys His Met Pro Thr Pro Glu Gln
272             260                 265                 270
274 Trp Thr Asn Val Phe Asn Pro Ala Tyr Ala Tyr Tyr Val Tyr Tyr Cys
275         275                 280                 285
277 Tyr Ala Asn Leu Tyr Thr Leu Asn Lys Leu Arg Glu Ser Lys Gly Met
278     290                 295                 300
280 Thr Thr Ile Lys Leu Arg Pro His Cys Gly Glu Ala Gly Asp Ile Asp
281 305                 310                 315                 320
283 His Leu Ala Ala Ala Phe Leu Thr Ser His Asn Ile Ala His Gly Val
284                 325                 330                 335
286 Asn Leu Lys Lys Ser Pro Val Leu Gln Tyr Leu Tyr Tyr Leu Ala Gln
287             340                 345                 350
289 Ile Gly Leu Ala Met Ser Pro Leu Ser Asn Asn Ser Met Phe Ile Asp
290         355                 360                 365
292 Tyr His Arg Asn Pro Phe Pro Thr Phe Phe Leu Arg Gly Leu Asn Val
293     370                 375                 380
295 Ser Leu Ser Thr Asp Asp Pro Leu Gln Ile His Leu Thr Lys Glu Pro
296 385                 390                 395                 400
298 Leu Val Glu Glu Tyr Ser Ile Ala Ala Ser Leu Trp Lys Leu Ser Ser
299                 405                 410                 415
301 Cys Asp Leu Cys Glu Ile Ala Arg Asn Ser Val Tyr Gln Ser Gly Phe
302             420                 425                 430
304 Ser His Arg Leu Lys Ser His Trp Ile Gly Arg Asn Tyr Tyr Lys Arg
305         435                 440                 445
307 Gly His Asp Gly Asn Asp Ile His Gln Thr Asn Val Pro His Ile Arg
308     450                 455                 460
310 Ile Glu Phe Arg His Thr Ile Trp Lys Glu Glu Met Glu Leu Ile His
311 465                 470                 475                 480
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314                 485                 490
316 <210> SEQ ID NO: 5
317 <211> LENGTH: 551
318 <212> TYPE: DNA
319 <213> ORGANISM: Glycine max
321 <220> FEATURE:
322 <221> NAME/KEY: unsure
323 <222> LOCATION: (290)
324 <223> OTHER INFORMATION: n= a, t, c, or g
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/21/2002
PATENT APPLICATION: US/10/019,633 TIME: 11:46:05

Input Set : A:\BB1386 US PCT substitute sequence listing.txt
Output Set: N:\CRF3\06212002\J019633.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:7; N Pos. 230,377,389,439,447,465,467,474,482,492,497,509,521,530,538
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Seq#:8; Xaa Pos. 56,81,105
Seq#:9; N Pos. 412,425,433,449,471,502,518,526,538,543,546,560,563,568,570
Seq#:9; N Pos. 572,575,576,577,586,594,595,608,619,642,657,660,661,672
Seq#:11; N Pos. 475,477,526
Seq#:13; N Pos. 4,5,9,12,14,17,18,24,45,54,57,63,69,73,74,81,85,94,118,119
Seq#:13; N Pos. 122,129,130,142,165,167,168,176,179,190,202,203,214,218,230
Seq#:13; N Pos. 235,241,244,250,277,293,315,320,328,357,367,411,497
Seq#:14; Xaa Pos. 15